

EXHIBIT 4

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

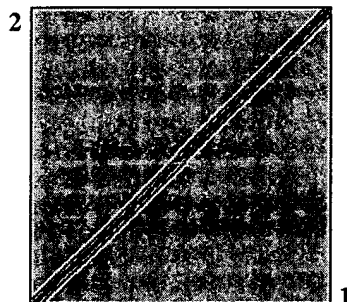
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option: **Standard**
 Masking character option: **X for protein, n for nucleotide** Masking color option: **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|1469860|dbj|BAA09787.1|leptin [Homo sapiens] >gi|4557715|ref|NP_000221.1| leptin precursor [Homo sapiens] >gi|730218|sp|P41159|LEP_HUMAN Leptin precursor (Obesity factor) (Obese protein) >gi|623332|gb|AAA60470.1| ob >gi|1226244|gb|AAC50400.1| obese protein >gi|1407583|dbj|BAA09839.1| ob protein [Homo sapiens] >gi|38174530|gb|AAH60830.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854318|gb|AAH69527.1| Leptin (obesity homolog, mouse) [Homo sapiens] >gi|46854679|gb|AAH69452.1| Leptin (obesity homolog, mouse) [Homo sapiens]...
 Length = 167 (1 .. 167)

Sequence 2: gi|55741433|ref|NP_999005.1|leptin [Sus scrofa] >gi|2498686|sp|Q29406|LEP_PIG Leptin precursor (Obesity factor) >gi|1402729|gb|AAB03458.1| leptin [Sus scrofa] >gi|1488299|gb|AAB05923.1| leptin >gi|2583209|gb|AAB82724.1| leptin [Sus scrofa] >gi|2981461|gb|AAC06303.1| leptin [Sus scrofa] >gi|3885981|gb|AAC78147.1| leptin [Sus scrofa] >gi|56001057|emb|CAI23842.1| leptin precursor [Sus scrofa domestica]
 Length = 167 (1 .. 167)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 280 bits (715), Expect = 3e-74
 Identities = 142/167 (85%), Positives = 153/167 (91%), Gaps = 0/167 (0%)

```

Query 1  MHWGTLCGFLWLWPYLFYVQAVPIQKVQDDTKTIKTIVTRINDISHTQSVSSKQKVTGL 60
          M G LC FLWLWPYL YV+AVPI +VQDDTKTIKTIVTRI+DISH QSVSSKQ+VTGL
Sbjct 1  MRCGPLCRFLWLWPYLSYVEAVPIWRVQDDTKTIKTIVTRISDISHMQSVSSKQRTVGL 60

Query 61  DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLP 120
          DFIPGLHP+L+LSKMDQTLA+YQQILTS+PSRNVIQISNDLENLRDLLH+LA SKSC LP
Sbjct 61  DFIPGLHPVLSLSKMDQTLAIYQQILTSLSRNVQISNDLENLRDLLHLLASSKSCPLP 120

Query 121  WASGLETLDLSGGVLEASGYSTEVVALSRLQGSQDMLWQLDLSPGC 167
          A LETL+SLGGVLEAS YSTEVVALSRLQG+LQDML QLDLSPGC
Sbjct 121  QARALETLESLSGGVLEASLYSTEVVALSRLQGALQDMLRQLDLSPGC 167
  
```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
0.321	0.135	0.415

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 295

Number of extensions: 101

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 167

Length of database: 1,565,033,500

Length adjustment: 124

Effective length of query: 43

Effective length of database: 1,565,033,376

Effective search space: 67296435168

Effective search space used: 67296435168

Neighboring words threshold: 9

X1: 16 (7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 73 (32.7 bits)